



1

SEQUENCE LISTING

<110> ZOLLER, MARK
LI, XIAODONG
STASZEWSKI, LENA
O'CONNELL, SHAWN
ZOZULYA, SERGEY
ADLER, JON
XU, HONG
ECHEVERRI, FERNANDO

<120> T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
IDENTIFICATION OF TASTE COMPOUNDS

<130> 078003-0291566

<140> 10/179,373

<141> 2002-06-26

<150> 60/300,434

<151> 2001-06-26

<150> 60/304,749

<151> 2001-07-13

<150> 60/310,493

<151> 2001-08-08

<150> 60/331,771

<151> 2001-11-21

<150> 60/339,472

<151> 2001-12-14

<150> 60/372,090

<151> 2002-04-15

<150> 60/374,143

<151> 2002-04-22

<160> 19

<170> PatentIn Ver. 2.1

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PDZIP sequence

<400> 1

Ser Val Ser Thr Trp

1

5

<210> 2
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<220>
 <221> MOD_RES
 <222> (1)
 <223> Thr or Arg

<220>
 <221> MOD_RES
 <222> (3)
 <223> Phe or Leu

<220>
 <221> MOD_RES
 <222> (4)
 <223> Arg, Gln or Pro

<220>
 <221> MOD_RES
 <222> (6)
 <223> Arg or Thr

<220>
 <221> MOD_RES
 <222> (7)
 <223> Ser, Pro or Val

<220>
 <221> MOD_RES
 <222> (8)
 <223> Val, Glu, Arg, Lys or Thr

<220>
 <221> MOD_RES
 <222> (11)
 <223> Ala or Glu

<220>
 <221> MOD_RES
 <222> (12)
 <223> Trp or Leu

<220>
 <221> MOD_RES
 <222> (13)
 <223> Arg, His or Gly

<400> 2
 Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
 1 5 10

<210> 3
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<220>
<221> MOD_RES
<222> (1)
<223> Leu or Gln

<220>
<221> MOD_RES
<222> (3)
<223> Glu, Gly or Thr

<220>
<221> MOD_RES
<222> (4)
<223> Asn, Arg or Cys

<220>
<221> MOD_RES
<222> (7)
<223> Arg or Glu

<220>
<221> MOD_RES
<222> (9)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (10)
<223> Cys, Gly or Phe

<220>
<221> MOD_RES
<222> (11)
<223> Val, Leu or Ile

<220>
<221> MOD_RES
<222> (13)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (14)
<223> Ala or Ser

<220>
<221> MOD_RES
<222> (15)

<223> Met or Leu

<400> 3

Xaa Pro Xaa Xaa Tyr Asn Xaa Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa
1 5 10 15

<210> 4

<211> 858

<212> PRT

<213> Rattus sp.

<400> 4

Met Pro Gly Leu Ala Ile Leu Gly Leu Ser Leu Ala Ala Phe Leu Glu
1 5 10 15

Leu Gly Met Gly Ser Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
20 25 30

Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Thr Thr Glu Glu
35 40 45

Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Gly Ile Leu Cys Thr Arg
50 55 60

Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
65 70 75 80

Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
85 90 95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Pro
100 105 110

Ser Leu Met Phe Met Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
115 120 125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
130 135 140

His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
145 150 155 160

Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
165 170 175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
180 185 190

Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
195 200 205

Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
210 215 220

Ile Phe Ser Gly Leu Ala Asn Ser Arg Gly Ile Cys Ile Ala His Glu
225 230 235 240

Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
 245 250 255
 Val Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
 260 265 270
 Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
 275 280 285
 Leu His Asp Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
 290 295 300
 Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
 305 310 315 320
 Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
 325 330 335
 Tyr Val Glu Thr Arg Leu Ala Leu Ala Ala Asp Pro Thr Phe Cys Ala
 340 345 350
 Ser Leu Lys Ala Glu Leu Asp Leu Glu Glu Arg Val Met Gly Pro Arg
 355 360 365
 Cys Ser Gln Cys Asp Tyr Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
 370 375 380
 Met Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
 385 390 395 400
 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
 405 410 415
 Cys Asn Val Ser His Cys His Thr Ser Glu Pro Val Gln Pro Trp Gln
 420 425 430
 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe Arg Ala Arg Asp Leu Thr
 435 440 445
 Leu Gln Phe Asp Ala Lys Gly Ser Val Asp Met Glu Tyr Asp Leu Lys
 450 455 460
 Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
 465 470 475 480
 Phe Asn Gly Thr Leu Gln Leu Gln His Ser Lys Met Tyr Trp Pro Gly
 485 490 495
 Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
 500 505 510
 Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
 515 520 525
 Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
 530 535 540

Pro Cys Gly Lys Asp Gln Trp Ser Pro Glu Lys Ser Thr Thr Cys Leu
 545 550 555 560
 Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Ser
 565 570 575
 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu Ala Ala Leu
 580 585 590
 Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
 595 600 605
 Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
 610 615 620
 Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser Cys Leu Ala
 625 630 635 640
 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
 645 650 655
 Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser
 660 665 670
 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu
 675 680 685
 Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr
 690 695 700
 Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro
 705 710 715 720
 Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly
 725 730 735
 Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly
 740 745 750
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
 755 760 765
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val
 770 775 780
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
 785 790 795 800
 Gly Ala Ile Leu Phe Cys Ala Leu Gly Ile Leu Ala Thr Phe His Leu
 805 810 815
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Glu Leu Asn Thr Gln Glu
 820 825 830
 Phe Phe Leu Gly Arg Ser Pro Lys Glu Ala Ser Asp Gly Asn Ser Gly
 835 840 845

Ser Ser Glu Ala Thr Arg Gly His Ser Glu
850 855

<210> 5
<211> 841
<212> PRT
<213> Homo sapiens

<400> 5
Met Leu Leu Cys Thr Ala Arg Leu Val Gly Leu Gln Leu Leu Ile Ser
1 5 10 15
Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
20 25 30
Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
35 40 45
Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
50 55 60
Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
65 70 75 80
Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
85 90 95
Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
100 105 110
Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu
115 120 125
Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile
130 135 140
Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser
145 150 155 160
Pro Phe Leu Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu
165 170 175
Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp
180 185 190
Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp
195 200 205
Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly
210 215 220
Val Gln Ala Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala
225 230 235 240
Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met
245 250 255

Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val
 260 265 270
 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
 275 280 285
 Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala
 290 295 300
 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met
 305 310 315 320
 Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala
 325 330 335
 Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys
 340 345 350
 His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
 355 360 365
 Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser
 370 375 380
 Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
 385 390 395 400
 His Gln Leu Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val
 405 410 415
 Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
 420 425 430
 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
 435 440 445
 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
 450 455 460
 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
 465 470 475 480
 Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val
 485 490 495
 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
 500 505 510
 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
 515 520 525
 Asn Lys Ser Asp Leu Tyr Arg Cys Gln Pro Cys Gly Lys Glu Glu Trp
 530 535 540
 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
 545 550 555 560

Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
 565 570 575
 Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
 580 585 590
 Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
 595 600 605
 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly
 610 615 620
 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
 625 630 635 640
 Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
 645 650 655
 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
 660 665 670
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
 675 680 685
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
 690 695 700
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
 705 710 715 720
 Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly
 725 730 735
 Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
 740 745 750
 Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe
 755 760 765
 Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp
 770 775 780
 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu
 785 790 795 800
 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
 805 810 815
 Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln
 820 825 830
 Asp Tyr Thr Arg Arg Cys Gly Ser Thr
 835 840

<210> 6

<211> 839

<212> PRT

<213> Homo sapiens

<400> 6

Met	Gly	Pro	Arg	Ala	Lys	Thr	Ile	Cys	Ser	Leu	Phe	Phe	Leu	Leu	Trp	1	5	10	15
Val	Leu	Ala	Glu	Pro	Ala	Glu	Asn	Ser	Asp	Phe	Tyr	Leu	Pro	Gly	Asp	20	25	30	
Tyr	Leu	Leu	Gly	Gly	Leu	Phe	Ser	Leu	His	Ala	Asn	Met	Lys	Gly	Ile	35	40	45	
Val	His	Leu	Asn	Phe	Leu	Gln	Val	Pro	Met	Cys	Lys	Glu	Tyr	Glu	Val	50	55	60	
Lys	Val	Ile	Gly	Tyr	Asn	Leu	Met	Gln	Ala	Met	Arg	Phe	Ala	Val	Glu	65	70	75	80
Glu	Ile	Asn	Asn	Asp	Ser	Ser	Leu	Leu	Pro	Gly	Val	Leu	Leu	Gly	Tyr	85	90	95	
Glu	Ile	Val	Asp	Val	Cys	Tyr	Ile	Ser	Asn	Asn	Val	Gln	Pro	Val	Leu	100	105	110	
Tyr	Phe	Leu	Ala	His	Glu	Asp	Asn	Leu	Leu	Pro	Ile	Gln	Glu	Asp	Tyr	115	120	125	
Ser	Asn	Tyr	Ile	Ser	Arg	Val	Val	Ala	Val	Ile	Gly	Pro	Asp	Asn	Ser	130	135	140	
Glu	Ser	Val	Met	Thr	Val	Ala	Asn	Phe	Leu	Ser	Leu	Phe	Leu	Leu	Pro	145	150	155	160
Gln	Ile	Thr	Tyr	Ser	Ala	Ile	Ser	Asp	Glu	Leu	Arg	Asp	Lys	Val	Arg	165	170	175	
Phe	Pro	Ala	Leu	Leu	Arg	Thr	Thr	Pro	Ser	Ala	Asp	His	His	Val	Glu	180	185	190	
Ala	Met	Val	Gln	Leu	Met	Leu	His	Phe	Arg	Trp	Asn	Trp	Ile	Ile	Val	195	200	205	
Leu	Val	Ser	Ser	Asp	Thr	Tyr	Gly	Arg	Asp	Asn	Gly	Gln	Leu	Leu	Gly	210	215	220	
Glu	Arg	Val	Ala	Arg	Arg	Asp	Ile	Cys	Ile	Ala	Phe	Gln	Glu	Thr	Leu	225	230	235	240
Pro	Thr	Leu	Gln	Pro	Asn	Gln	Asn	Met	Thr	Ser	Glu	Glu	Arg	Gln	Arg	245	250	255	
Leu	Val	Thr	Ile	Val	Asp	Lys	Leu	Gln	Gln	Ser	Thr	Ala	Arg	Val	Val	260	265	270	
Val	Val	Phe	Ser	Pro	Asp	Leu	Thr	Leu	Tyr	His	Phe	Phe	Asn	Glu	Val	275	280	285	

Leu Arg Gln Asn Phe Thr Gly Ala Val Trp Ile Ala Ser Glu Ser Trp
 290 295 300
 Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu Gly His Leu Gly
 305 310 315 320
 Thr Phe Leu Gly Ile Thr Ile Gln Ser Val Pro Ile Pro Gly Phe Ser
 325 330 335
 Glu Phe Arg Glu Trp Gly Pro Gln Ala Gly Pro Pro Pro Leu Ser Arg
 340 345 350
 Thr Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn
 355 360 365
 Ala Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val
 370 375 380
 Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His
 385 390 395 400
 Ser Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr
 405 410 415
 Pro Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu
 420 425 430
 Asp His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu
 435 440 445
 Glu Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser
 450 455 460
 Val Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Gln Asp
 465 470 475 480
 Ile Ser Trp His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser
 485 490 495
 Lys Arg Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val
 500 505 510
 Cys Cys Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His
 515 520 525
 Thr Glu Asp Glu Tyr Glu Cys Gln Ala Cys Pro Asn Asn Glu Trp Ser
 530 535 540
 Tyr Gln Ser Glu Thr Ser Cys Phe Lys Arg Gln Leu Val Phe Leu Glu
 545 550 555 560
 Trp His Glu Ala Pro Thr Ile Ala Val Ala Leu Leu Ala Ala Leu Gly
 565 570 575
 Phe Leu Ser Thr Leu Ala Ile Leu Val Ile Phe Trp Arg His Phe Gln
 580 585 590

Thr Pro Ile Val Arg Ser Ala Gly Gly Pro Met Cys Phe Leu Met Leu
 595 600 605
 Thr Leu Leu Leu Val Ala Tyr Met Val Val Pro Val Tyr Val Gly Pro
 610 615 620
 Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys
 625 630 635 640
 Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val
 645 650 655
 Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp
 660 665 670
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu
 675 680 685
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Thr Gly Leu Ser Pro
 690 695 700
 Thr Thr Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys
 705 710 715 720
 Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu
 725 730 735
 Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu
 740 745 750
 Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe
 755 760 765
 Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser
 770 775 780
 Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu
 785 790 795 800
 Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu
 805 810 815
 Phe Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln
 820 825 830
 Gly Tyr Thr Met Arg Arg Asp
 835

<210> 7

<211> 852

<212> PRT

<213> Homo sapiens

<400> 7

Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His
 1 5 10 15

Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys
 20 25 30
 Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
 35 40 45
 Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
 50 55 60
 Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
 65 70 75 80
 Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
 85 90 95
 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
 100 105 110
 Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
 115 120 125
 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
 130 135 140
 His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
 145 150 155 160
 Leu Met Pro Gln Val Ser Tyr Gly Ala Ser Met Glu Leu Leu Ser Ala
 165 170 175
 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
 180 185 190
 Gln Leu Thr Ala Ala Ala Glu Leu Leu Gln Glu Phe Gly Trp Asn Trp
 195 200 205
 Val Ala Ala Leu Gly Ser Asp Asp Glu Tyr Gly Arg Gln Gly Leu Ser
 210 215 220
 Ile Phe Ser Ala Leu Ala Ala Ala Arg Gly Ile Cys Ile Ala His Glu
 225 230 235 240
 Gly Leu Val Pro Leu Pro Arg Ala Asp Asp Ser Arg Leu Gly Lys Val
 245 250 255
 Gln Asp Val Leu His Gln Val Asn Gln Ser Ser Val Gln Val Val Leu
 260 265 270
 Leu Phe Ala Ser Val His Ala Ala His Ala Leu Phe Asn Tyr Ser Ile
 275 280 285
 Ser Ser Arg Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ala Trp Leu
 290 295 300
 Thr Ser Asp Leu Val Met Gly Leu Pro Gly Met Ala Gln Met Gly Thr
 305 310 315 320

Val Leu Gly Phe Leu Gln Arg Gly Ala Gln Leu His Glu Phe Pro Gln
 325 330 335
 Tyr Val Lys Thr His Leu Ala Leu Ala Thr Asp Pro Ala Phe Cys Ser
 340 345 350
 Ala Leu Gly Glu Arg Glu Gln Gly Leu Glu Glu Asp Val Val Gly Gln
 355 360 365
 Arg Cys Pro Gln Cys Asp Cys Ile Thr Leu Gln Asn Val Ser Ala Gly
 370 375 380
 Leu Asn His His Gln Thr Phe Ser Val Tyr Ala Ala Val Tyr Ser Val
 385 390 395 400
 Ala Gln Ala Leu His Asn Thr Leu Gln Cys Asn Ala Ser Gly Cys Pro
 405 410 415
 Ala Gln Asp Pro Val Lys Pro Trp Gln Leu Leu Glu Asn Met Tyr Asn
 420 425 430
 Leu Thr Phe His Val Gly Gly Leu Pro Leu Arg Phe Asp Ser Ser Gly
 435 440 445
 Asn Val Asp Met Glu Tyr Asp Leu Lys Leu Trp Val Trp Gln Gly Ser
 450 455 460
 Val Pro Arg Leu His Asp Val Gly Arg Phe Asn Gly Ser Leu Arg Thr
 465 470 475 480
 Glu Arg Leu Lys Ile Arg Trp His Thr Ser Asp Asn Gln Lys Pro Val
 485 490 495
 Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly Gln Val Arg Arg Val Lys
 500 505 510
 Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp Cys Glu Ala Gly Ser
 515 520 525
 Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys Thr Phe Cys Gly Gln Asp
 530 535 540
 Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys Phe Arg Arg Arg Ser Arg
 545 550 555 560
 Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Leu Leu Leu Leu Leu
 565 570 575
 Ser Leu Ala Leu Gly Leu Val Leu Ala Ala Leu Gly Leu Phe Val His
 580 585 590
 His Arg Asp Ser Pro Leu Val Gln Ala Ser Gly Gly Pro Leu Ala Cys
 595 600 605
 Phe Gly Leu Val Cys Leu Gly Leu Val Cys Leu Ser Val Leu Leu Phe
 610 615 620

Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu Ala Gln Gln Pro Leu Ser
 625 630 635 640
 His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu Phe Leu Gln Ala Ala
 645 650 655
 Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser Trp Ala Asp Arg Leu
 660 665 670
 Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp Leu Val Val Leu Leu Ala
 675 680 685
 Met Leu Val Glu Val Ala Leu Cys Thr Trp Tyr Leu Val Ala Phe Pro
 690 695 700
 Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val
 705 710 715 720
 His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr
 725 730 735
 Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg
 740 745 750
 Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met
 755 760 765
 Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn
 770 775 780
 Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu
 785 790 795 800
 Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu
 805 810 815
 Leu Met Arg Gln Pro Gly Leu Asn Thr Pro Glu Phe Phe Leu Gly Gly
 820 825 830
 Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln
 835 840 845
 Gly Lys His Glu
 850

<210> 8

<211> 2526

<212> DNA

<213> Homo sapiens

<400> 8

atgctgctct gcacggctcg cctggctggc ctgcagcttc tcatttcctg ctgctgggcc 60
 ttgctgccc atagcacgga gtcttctcct gacttcaccc tccccggaga ttacctcctg 120
 gcaggcctgt tccctctcca ttctggctgt ctgcaggtga ggcacagacc cgaggtgacc 180
 ctgtgtgaca ggtctttag cttcaatgag catggctacc acctcttcca ggctatgcgg 240
 cttggggttg aggagataaa caactccacg gccctgctgc ccaacatcac cctgggggtac 300
 cagctgtatg atgtgtgttc tgactctgcc aatgtgtatg ccacgctgag agtgcctccc 360

```

ctgccagggc aacaccacat agagctccaa ggagaccttc tccactattc ccctacggtg 420
ctggcagtga ttgggcctga cagcaccaac cgtgctgcca ccacagccgc cctgctgagc 480
cctttcctgg tgcccatgat tagctatgcg gccagcagcg agacgctcag cgtgaagcgg 540
cagtatccct ctttcctgcg caccatcccc aatgacaagt accaggtgga gaccatggtg 600
ctgctgctgc agaagtccgg gtggacctgg atctctctgg ttggcagcag tgacgactat 660
gggcagctag ggggtgcaggc actggagaac caggccactg gtcaggggat ctgcattgct 720
ttcaaggaca tcatgccctt ctctgccagc gtgggcgatg agaggatgca gtgcctcatg 780
cgccacctgg cccaggccgg ggccaccgtc gtggttgttt tttccagccg gcagttggcc 840
aggggtgttt tccagtcctg ggtgctgacc aacctgactg gcaaggtgtg ggtgcctca 900
gaagcctggg cctctccag gcacatcact ggggtgcccg ggatccagcg cattgggatg 960
gtgctgggcg tggccatcca gaagagggct gtccctggcc tgaaggcgtt tgaagaagcc 1020
tatgccggg cagacaagaa ggcccctagg ccttgccaca agggctcctg gtgcagcagc 1080
aatcagctct gcagagaatg ccaagctttc atggcacaca cgatgcccaa gctcaaagcc 1140
ttctccatga gttctgccta caacgcatac cgggctgtgt atgcggtggc ccatggcctc 1200
caccagctcc tgggctgtgc ctctggagct tgttccaggg gccgagtcta cccctggcag 1260
cttttgagc agatccacaa ggtgcatttc cttctacaca aggacactgt ggcgtttaat 1320
gacaacagag atccccctag tagctataac ataattgcct gggactggaa tggacccaag 1380
tggaccttca agtgcctcgg ttccctccaca tggctccag ttccagctaaa cataaatgag 1440
acaaaaatcc agtggcacgg aaaggacaac caggtgccta agtctgtgtg ttccagcgac 1500
tgtcttgaag ggcaccagcg agtggttacg ggtttccatc actgctgctt tgagtgtgtg 1560
ccctgtgggg ctgggacctt cctcaacaag agtgacctct acagatgcca gccttgtggg 1620
aaagaagagt gggcacctga ggggaagccag acctgcttcc cgcgcactgt ggtgtttttg 1680
gctttgcgtg agcacacctc ttgggtgctg ctggcagcta acacgctgct gctgctgctg 1740
ctgcttggga ctgctggcct gtttgcctgg cacctagaca cccctgtggt gaggtcagca 1800
gggggcccgc tgtctttct tatgctgggc tccctggcag caggtagtgg cagcctctat 1860
ggcttctttg gggaacccac aaggcctgcg tgcctgtac gccaggccct ctttgcctt 1920
ggtttcacca tcttctgtc ctgcctgaca gttcgtcat tccaaactaat catcatcttc 1980
aagttttcca ccaaggtacc tacattctac cacgcctggg tccaaaacca cgggtgctggc 2040
ctgtttgtga tgatcagctc agcggcccg ctgcttatct gtctaacttg gctggtggtg 2100
tggacccccc tgctgctag ggaataccag cgcttcccc atctggtgat gcttgagtgc 2160
acagagacca actccctggg cttcatactg gccttccctt acaatggcct cctctccatc 2220
agtgcctttg cctgcagcta cctgggtaag gacttgccag agaactacaa cgaggccaaa 2280
tgtgtcacct tcagcctgct cttcaacttc gtgtcctgga tcgccttctt caccacggcc 2340
agcgtctacg acggcaagta cctgcctgcg gccaacatga tggctgggct gagcagcctg 2400
agcagcggct tcggtgggta ttttctgcct aagtgtacg tgatcctctg ccgccagac 2460
ctcaacagca cagagcactt ccaggcctcc attcaggact acacgaggcg ctgcggctcc 2520
acctga 2526

```

<210> 9

<211> 2559

<212> DNA

<213> Homo sapiens

<400> 9

```

atgctgggccc ctgctgtcct gggcctcagc ctctgggctc tccctgacccc tgggacgggg 60
gccccattgt gctgtcaca gcaacttagg atgaaggggg actacgtgct ggggggggctg 120
ttccccctgg gcgaggccga ggaggctggc ctccgcagcc ggacacggcc cagcagccct 180
gtgtgcacca ggttctctc aaacggcctg cctctggcac tggccatgaa aatggccgtg 240
gaggagatca acaacaagtc ggatctgctg cccgggctgc gcctgggcta cgacctcttt 300
gatacgtgct cggagcctgt ggtggccatg aagcccagcc tcatgttctt ggccaaggca 360
ggcagcccg acatcgccgc ctactgcaac tacacgagt accagccccg tgtgctggct 420
gtcatcgggc cccactcgtc agagctcgcc atggtcaccg gcaagttctt cagcttcttc 480
ctcatgcccc aggtcagcta cgggtgctagc atggagctgc tgagcgcccc ggagaccttc 540
ccctccttct tccgcaccgt gccagcgac cgtgtgcagc tgacggccgc cgcggagctg 600
ctgcaggagt tcggctggaa ctgggtggcc gccctgggca gcgacgacga gtacggccgg 660
cagggcctga gcatcttctc ggccctggcc gcggcacgcg gcatctgcat cgcgcacgag 720
ggcctggtgc cgctgccccg tgccgatgac tcgcggctgg ggaaggtgca ggacgtcctg 780

```


caccaggtga	accagagcag	cgtgcaggtg	gtgctgctgt	tcgcctccgt	gcacgccgcc	840
cacgcctct	tcaactacag	catcagcagc	aggctctcgc	ccaaggtgtg	ggtggccagc	900
gaggcctggc	tgacctctga	cctggtcatg	gggctgccc	gcatggccca	gatgggcacg	960
gtgcttggt	tcctccagag	gggtgcccag	ctgcacgagt	tccccagta	cgtgaagacg	1020
cacctggccc	tggccaccga	cccggccttc	tgctctgccc	tgggcgagag	ggagcagggt	1080
ctggaggagg	acgtggtggg	ccagcgctgc	ccgcagtgtg	actgcacac	gctgcagaac	1140
gtgagcgag	ggctaaatca	ccaccagacg	ttctctgtct	acgcagctgt	gtatagcgtg	1200
gcccaggccc	tgcacaacac	tcttcagtgc	aacgcctcag	gctgccccgc	gcaggacccc	1260
gtgaagccct	ggcagctcct	ggagaacatg	tacaacctga	ccttccacgt	gggcgggctg	1320
ccgctgcggt	tcgacagcag	cggaaacgtg	gacatggagt	acgacctgaa	gctgtgggtg	1380
tggcagggct	cagtgcacag	gctccacgac	gtgggcaggt	tcaacggcag	cctcaggaca	1440
gagcgccctg	agatccgctg	gcacacgtct	gacaaccaga	agcccgtgtc	ccggtgctcg	1500
cggcagtgcc	aggagggcca	ggtgcgcggg	gtcaaggggg	tccactcctg	ctgctacgac	1560
tgtgtggact	gcgaggcggg	cagctaccgg	caaaaccagg	acgacatcgc	ctgcaccttt	1620
tgtggccagg	atgagtggtc	cccggagcga	agcacacgct	gcttccgccc	caggctctcg	1680
ttcctggcat	ggggcgagcc	ggctgtgctg	ctgctgctcc	tgctgctgag	cctggcgctg	1740
ggccttgctg	tggctgcttt	ggggctgttc	gttcaccatc	gggacagccc	actggttcag	1800
gcctcggggg	ggcccctggc	ctgctttggc	ctgggtgtgc	tgggcctggt	ctgcctcagc	1860
gtcctcctgt	tccttgggca	gcccagccct	gccgatgccc	tggcccagca	gcccttgtcc	1920
cacctcccgc	tcacgggctg	cctgagcaca	ctcttctcgc	aggcgccga	gatctctgtg	1980
gagtcagaac	tgctctctgag	ctgggcagac	cggctgagtg	gctgcctgcg	ggggccctgg	2040
gcctggctgg	tgggtgctgct	ggccatgctg	gtggaggctg	cactgtgcac	ctggtacctg	2100
gtggccttcc	cgccggaggt	ggtgacggac	tggcacatgc	tgcccacgga	ggcgctgggtg	2160
cactgccgca	cagctcctg	ggtcagcttc	ggcctagcgc	acgccacca	tgccacgctg	2220
gcctttctct	gcttctctgg	cactttcctg	gtgcggagcc	agccgggctg	ctacaaccgt	2280
gcccgtggcc	tcacctttgc	catgctggcc	tacttcatca	cctgggtctc	ctttgtgccc	2340
ctcctggcca	atgtgcaggt	ggtcctcagg	cccgcgctgc	agatgggcgc	cctcctgctc	2400
tgtgtcctgg	gcatcctggc	tgccctccac	ctgcccagg	gttacctgct	catgcggcag	2460
ccagggtcca	acacccccga	gttcttctctg	ggaggggggc	ctggggatgc	ccaaggccag	2520
aatgacggga	acacaggaaa	tcaggggaaa	catgagtga			2559

<210> 10

<211> 2519

<212> DNA

<213> Homo sapiens

<400> 10

atggggccca	gggcaaagac	catctgctcc	ctgtttcttc	tcctatgggt	cctggctgag	60
ccggctgaga	actcggactt	ctacctgcct	ggggattacc	tcctgggtgg	cctcttctcc	120
ctccatgcca	acatgaaggg	cattgttcac	cttaacttcc	tgcagggtgcc	catgtgcaag	180
gagtatgaag	tgaaggatgat	aggctacaac	ctcatgcagg	ccatgcgctt	cgcggtggag	240
gagatcaaca	atgacagcag	cctgctgcct	ggtgtgctgc	tgggctatga	gatcgtggat	300
gtgtgtctaca	tctccaacaa	tgtccagccg	gtgctctact	tcctggcaca	cgaggacaac	360
ctccttccca	tccaagagga	ctacagtaac	tacatttccc	gtgtgggtggc	tgtcattggc	420
cctgacaact	ccgagtctgt	catgactgtg	gccaaacttc	tcctccctatt	tctccttcca	480
cagatcacct	acagcgccat	cagcgatgag	ctgcgagaca	aggtgcgctt	cccggctttg	540
ctgcgtacca	caccagcgc	cgaccaccac	gtcgaggcca	tgggtgcagct	gatgtgcac	600
ttccgctgga	actggatcat	tgtgctgggt	agcagcgaca	cctatggccg	cgacaatggc	660
agctgcttgg	cgagcgctg	gcccggcgcg	acatctgcat	cgccctccag	gagacgctgc	720
ccacactgca	gccccaccag	aacatgacgt	cagaggagcg	ccagcgccctg	gtgaccattg	780
tggacaagct	gcagcagagc	acagcgcgcg	tcgtggctcgt	gttctcgccc	gacctgaccc	840
tgtaccactt	cttcaatgag	gtgctgcgcc	agaacttcac	gggcgcgctg	tggatcgcc	900
ccgagtcctg	ggccatcgac	ccggtcctgc	acaacctcac	ggagctgggc	cacttgggca	960
ccttcttggg	catcaccatc	cagagcgtgc	ccatcccggg	cttcagttag	ttccgcgagt	1020
ggggccca	ggctgggccc	ccacccctca	cgaggaccag	ccagagctat	acctgcaacc	1080
aggagtgcga	caactgcctg	aacgccacct	tgtccttcaa	caccattctc	aggctctctg	1140
gggagcggtg	cgtctacagc	gtgtactctg	cggctctatgc	tgtggcccat	gccctgcaca	1200

gcctcctcgg	ctgtgacaaa	agcacctgca	ccaagagggg	ggctaccccc	tggcagctgc	1260
ttgaggagat	ctggaagggtc	aacttcactc	tcttggaacca	ccaaatcttc	ttcgacccgc	1320
aaggggacgt	ggctctgcac	ttggagattg	tccagtgga	atgggaccgg	agccagaatc	1380
ccttccagag	cgtcgctcc	tactaccccc	tgcagcgaca	gctgaagaac	atccaagaca	1440
tctcctggca	caccgtcaac	aacacgatcc	ctatgtccat	gtgttccaag	agggtgccagt	1500
cagggcaaaa	gaagaagcct	gtgggcatcc	acgtctgctg	cttcgagtgc	atcgactgcc	1560
ttcccggcac	cttctcaac	cacactgaag	atgaatatga	atgccaggcc	tgcccgaata	1620
acgagtgggc	ctaccagagt	gagacctcct	gcttcaagcg	gcagctgggc	ttcctggaat	1680
ggcatgaggg	accacccatc	gctgtggccc	tgttgccgc	cctgggcttc	ctcagcacc	1740
tggccatcct	ggtgatattc	tggaggcact	tccagacacc	catagtctgc	tgggctgggg	1800
gccccatgtg	cttctgatg	ctgacactgc	tgttggtggc	atacatgggtg	gtcccgggtg	1860
acgtggggcc	gccaagggtc	tccacctgcc	tctgcccga	ggccctcttt	ccctctgtct	1920
tcacaatttg	catctcctgt	atcgccgtgc	gttctttcca	gatcgtctgc	gccttcaaga	1980
tggccagccg	cttcccacgc	gcctacagct	actgggtccg	ctaccagggg	ccctacgtct	2040
ctatggcatt	tatcacggta	ctcaaaatgg	tcatgtgtgt	aattggcatg	ctggccacgg	2100
gcctcagtc	caccacccgt	actgaccccg	atgacccaa	gatcacaatt	gtctcctgta	2160
accccaacta	ccgcaacagc	ctgctgttca	acaccagcct	ggacctgctg	ctctcagttg	2220
tgggtttcag	cttcgcctac	atgggcaaa	agctgcccac	caactacaac	gaggccaagt	2280
tcataccct	cagcatgacc	ttctatttca	cctcatccgt	ctccctctgc	accttcattg	2340
ctgcctacag	cggggtgctg	gtcaccatcg	tggacctctt	ggtcactgtg	ctcaacctcc	2400
tggccatcag	cctgggctac	ttcggcccca	agtgtacat	gatcctcttc	taccgggagc	2460
gcaacacgcc	cgctacttcc	aacagcatga	tccagggcta	caccatgagg	agggactag	2519

<210> 11

<211> 2577

<212> DNA

<213> Rattus sp.

<400> 11

atgccggggt	tggctatctt	gggcctcagt	ctggctgctt	tcctggagct	tgggatgggg	60
tcctctttgt	gtctgtcaca	gcaattcaag	gcacaagggg	actatatatt	gggtggacta	120
tttcccctgg	gcacaactga	ggaggccact	ctcaaccaga	gaacacagcc	caacggcatc	180
ctatgtacca	ggttctcgcc	ccttgggttg	ttcctggcca	tggctatgaa	gatggctgta	240
gaggagatca	acaatggatc	tgccttgctc	cctgggctgc	gactgggcta	tgacctgttt	300
gacacatgct	cagagccagt	ggtcaccatg	aagcccagcc	tcatgttcat	ggccaagggtg	360
ggaagtcaaa	gcattgctgc	ctactgcaac	tacacacagt	accaaccccg	tgtgctggct	420
gtcattgggc	cccactcatc	agagcttgcc	ctcattacag	gcaagttctt	cagcttcttc	480
ctcatgccac	aggtcagcta	tagtgccagc	atggatcggc	taagtgaccg	ggaaacattt	540
ccatccttct	tccgcacagt	gcccagtgac	cgggtgcagc	tgcaggccgt	tgtgacactg	600
ttgcagaatt	tcagctggaa	ctgggtggct	gccttaggta	gtgatgatga	ctatggccgg	660
gaaggctctga	gcatcttttc	tggcttgccc	aactcacgag	gtatctgcat	tgcacacgag	720
ggcctgggtg	cacaacatga	cactagtggc	caacaattgg	gcaagggtgg	ggatgtgcta	780
cgccaagtga	accaaagcaa	agtacagggtg	gtgggtgctg	ttgcatctgc	ccgtgctgtc	840
tactcccttt	ttagctacag	catccttcat	gacctctcac	ccaagggtatg	ggtggccagt	900
gagtcctggc	tgacctctga	cctggctcatg	acacttccca	atattgcccg	tgtgggcact	960
gttcttgggt	ttctgcagcg	cggtgcccta	ctgcctgaat	tttcccatta	tgtggagact	1020
cgcttggccc	tagctgctga	cccaacattc	tgtgcctccc	tgaaagctga	gttggatctg	1080
gaggagcgcg	tgatggggcc	acgtgtttca	caatgtgact	acatcatgct	acagaacctg	1140
tcactctggg	tgatgcagaa	cctatcagct	gggcagttgc	accaccaa	atttgcaacc	1200
tatgcagctg	tgtacagtgt	ggctcaggcc	cttcacaaca	ccctgcagtg	caatgtctca	1260
cattgccaca	catcagagcc	tgttcaaccc	tggcagctcc	tggagaacat	gtacaatatg	1320
agtttccgtg	ctcgagactt	gacactgcag	ttttagtgcca	aagggagtgt	agacatggaa	1380
tatgacctga	agatgtgggt	gtggcagagc	cctacacctg	tactacatac	tgtaggcacc	1440
ttcaacggca	cccttcagct	gcagcactcg	aaaatgtatt	ggccaggcaa	ccagggtgcca	1500
gtctcccagt	gctcccggca	gtgcaaagat	ggccagggtgc	gcagagtaaa	gggctttcat	1560
tcctgctgct	atgactgtgt	ggactgcaag	gcaggagct	accggaagca	tccagatgac	1620
ttcacctgta	ctccatgtgg	caaggatcag	tgggtcccag	aaaaaagcac	aacctgctta	1680

```

cctcgaggc ccaagtttct ggcttggggg gagccagctg tgctgtcact tctcctgctg 1740
ctttgcctgg tgctgggcct gacactggct gccctggggc tctttgtcca ctactgggac 1800
agccctcttg ttcaggcctc aggtgggtca ctgttctgct ttggcctgat ctgcctaggc 1860
ctcttctgcc tcagtgtcct tctgttccca ggacgaccac gctctgccag ctgccttgcc 1920
caacaaccaa tggctcacct ccctctcaca ggctgcctga gcacactctt cctgcaagca 1980
gccgagatct ttgtggagtc tgagctgcca ctgagttggg caaactggct ctgcagctac 2040
cttcggggcc cctgggcttg gctgggtgga ctgctggcca ctcttgtgga ggctgcacta 2100
tgtgcctggg acttgatggc tttccctcca gaggtgggta cagattggca ggtgctgccc 2160
acggaggtag tggaacactg ccgcatgcgt tcctgggtca gcctgggctt ggtgcacatc 2220
accaatgcag tgtagcttt cctctgcttt ctgggcactt tcctgggtaca gagccagcct 2280
ggtcgctata accgtgcccg tggcctcacc ttcgcatgc tagcttattt catcatctgg 2340
gtctcttttg tgccctcctt ggctaagtgt caggtggcct accagccagc tgtgcagatg 2400
ggtgctatct tattctgtgc cctgggcacg ctggccacct tccacctgcc caaatgctat 2460
gtacttctgt ggctgccaga gctcaacacc caggagtctt tcctgggaag gagccccaag 2520
gaagcatcag atgggaatag tggtagtagt gaggcaactc ggggacacag tgaatga 2577

```

<210> 12

<211> 137

<212> PRT

<213> Fugu rubripes

<400> 12

```

Pro Ser Pro Phe Arg Asp Ile Val Ser Tyr Pro Asp Lys Ile Ile Leu
  1             5             10             15

```

```

Gly Cys Phe Met Asn Leu Lys Thr Ser Ser Val Ser Phe Val Leu Leu
      20             25             30

```

```

Leu Leu Leu Cys Leu Leu Cys Phe Ile Phe Ser Tyr Met Gly Lys Asp
      35             40             45

```

```

Leu Pro Lys Asn Tyr Asn Glu Ala Lys Ala Ile Thr Phe Cys Leu Leu
      50             55             60

```

```

Leu Leu Ile Leu Thr Trp Ile Ile Phe Thr Thr Ala Ser Leu Leu Tyr
      65             70             75             80

```

```

Gln Gly Lys Tyr Ile His Ser Leu Asn Ala Leu Ala Val Leu Ser Ser
      85             90             95

```

```

Ile Tyr Ser Phe Leu Leu Trp Tyr Phe Leu Pro Lys Cys Tyr Ile Ile
      100            105            110

```

```

Ile Phe Gln Pro Gln Lys Asn Thr Gln Lys Tyr Phe Gln Gly Leu Ile
      115            120            125

```

```

Gln Asp Tyr Thr Lys Thr Ile Ser Gln
      130            135

```

<210> 13

<211> 242

<212> PRT

<213> Tetraodon cutcutia

<220>

<221> MOD_RES.

<222> (120)..(121)
 <223> Any amino acid

<400> 13

Phe Ala Val Asn Tyr Asn Thr Pro Val Val Arg Ser Ala Gly Gly Pro
 1 5 10 15
 Met Cys Phe Leu Ile Leu Gly Cys Leu Ser Leu Cys Ser Ile Ser Val
 20 25 30
 Phe Phe Tyr Phe Glu Arg Pro Thr Glu Ala Phe Cys Ile Leu Arg Phe
 35 40 45
 Met Pro Phe Leu Leu Phe Tyr Ala Val Cys Leu Ala Cys Phe Ala Val
 50 55 60
 Arg Ser Phe Gln Ile Val Ile Ile Phe Lys Ile Ala Ala Lys Phe Pro
 65 70 75 80
 Arg Val His Ser Trp Trp Met Lys Tyr His Gly Gln Trp Leu Val Ile
 85 90 95
 Ser Met Thr Phe Val Leu Gln Ala Val Val Ile Val Ile Gly Phe Ser
 100 105 110
 Ser Asn Pro Pro Leu Pro Tyr Xaa Xaa Phe Val Ser Tyr Pro Asp Lys
 115 120 125
 Ile Ile Leu Gly Cys Asp Val Asn Leu Asn Met Ala Ser Thr Ser Phe
 130 135 140
 Phe Leu Leu Leu Leu Leu Cys Ile Leu Cys Phe Thr Phe Ser Tyr Met
 145 150 155 160
 Gly Lys Asp Leu Pro Lys Asn Tyr Asn Glu Ala Lys Ala Ile Thr Phe
 165 170 175
 Cys Leu Leu Leu Leu Ile Leu Thr Trp Ile Ile Phe Ala Thr Ala Phe
 180 185 190
 Met Leu Tyr His Gly Lys Tyr Ile His Thr Leu Asn Ala Leu Ala Val
 195 200 205
 Leu Ser Ser Ala Tyr Cys Phe Leu Leu Trp Tyr Phe Leu Pro Lys Cys
 210 215 220
 Tyr Ile Ile Ile Phe Gln Pro His Lys Asn Thr Gln Lys Tyr Phe Gln
 225 230 235 240
 Leu Ser

<210> 14
 <211> 165
 <212> PRT
 <213> Fugu rubripes

<400> 14

Lys Lys Gln Gly Pro Glu Val Asp Ile Phe Ile Val Ser Val Thr Ile
 1 5 10 15

Leu Cys Ile Ser Val Leu Gly Val Ala Val Gly Pro Pro Glu Pro Ser
 20 25 30

Gln Asp Leu Asp Phe Tyr Met Asp Ser Ile Val Leu Glu Cys Ser Asn
 35 40 45

Thr Leu Ser Pro Gly Ser Phe Ile Glu Leu Cys Tyr Val Cys Val Leu
 50 55 60

Ser Val Leu Cys Phe Phe Phe Ser Tyr Met Gly Lys Asp Leu Pro Ala
 65 70 75 80

Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Met Val Tyr Met
 85 90 95

Ile Ser Trp Ile Ser Phe Phe Thr Val Tyr Leu Ile Ser Arg Gly Pro
 100 105 110

Phe Thr Val Ala Ala Tyr Val Cys Ala Thr Leu Val Ser Val Leu Ala
 115 120 125

Phe Phe Gly Gly Tyr Phe Leu Pro Lys Ile Tyr Ile Ile Val Leu Lys
 130 135 140

Pro Gln Met Asn Thr Thr Ala His Phe Gln Asn Cys Ile Gln Met Tyr
 145 150 155 160

Thr Met Ser Lys Gln
 165

<210> 15

<211> 236

<212> PRT

<213> Tetraodon cutcutia

<220>

<221> MOD_RES

<222> (8)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (15)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (59)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (62)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (76)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (117)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (128)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (136)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (168)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (173)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (175)..(176)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (203)

<223> Any amino acid

<220>

<221> MOD_RES

<222> (226)

<223> Any amino acid

<400> 15

Ala	Pro	Lys	Ser	Ser	Gln	Arg	Xaa	Leu	Arg	Arg	Thr	Arg	Leu	Xaa	Leu
1				5					10					15	

Glu	Trp	Asp	His	Pro	Met	Ser	Val	Ala	Leu	Leu	Phe	Phe	Leu	Val	Cys
			20					25					30		

Cys	Leu	Leu	Met	Thr	Ser	Ser	Ser	Ala	Val	Ile	Leu	Leu	Leu	Asn	Ile
	35						40						45		

Asn Thr Pro Val Ala Lys Ser Ala Gly Gly Xaa Thr Cys Xaa Leu Lys
 50 55 60
 Leu Ala Ala Leu Thr Ala Ala Ala Met Ser Ser Xaa Cys His Phe Gly
 65 70 75 80
 Gln Pro Ser Pro Leu Ala Ser Lys Leu Lys Gln Pro Gln Phe Thr Phe
 85 90 95
 Ser Phe Thr Val Cys Leu Ala Cys Asn Arg Cys Ala Leu Ala Thr Gly
 100 105 110
 His Leu His Phe Xaa Ile Arg Val Ala Leu Pro Pro Ala Tyr Asn Xaa
 115 120 125
 Trp Ala Lys Asn His Gly Pro Xaa Ala Thr Ile Phe Ile Ala Ser Ala
 130 135 140
 Ala Ile Leu Cys Val Leu Cys Leu Arg Val Ala Val Gly Pro Pro Gln
 145 150 155 160
 Pro Ser Gln Asx Leu Asx Phe Xaa Thr Asn Ser Ile Xaa Leu Xaa Xaa
 165 170 175
 Ser Asn Thr Leu Ser Pro Gly Ser Phe Val Glu Leu Cys Asn Val Ser
 180 185 190
 Leu Leu Ser Ala Val Cys Phe Val Phe Ser Xaa Met Gly Lys Asx Leu
 195 200 205
 Pro Ala Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Met Val
 210 215 220
 Asn Xaa Ile Ser Trp Ile Ser Phe Phe Thr Val Tyr
 225 230 235

<210> 16
 <211> 840
 <212> PRT
 <213> Rattus sp.

<400> 16
 Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Val Tyr
 1 5 10 15
 Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly Phe Ser
 20 25 30
 Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp
 35 40 45
 Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro
 50 55 60
 Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe
 65 70 75 80

Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr
 85 90 95
 Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr
 100 105 110
 Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile
 115 120 125
 Gln Lys Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Phe Ile Gly
 130 135 140
 Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu Gly Pro
 145 150 155 160
 Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Val Leu Ser
 165 170 175
 Ala Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Arg
 180 185 190
 His Gln Val Glu Val Met Val Gln Leu Leu Gln Ser Phe Gly Trp Val
 195 200 205
 Trp Ile Ser Leu Ile Gly Ser Tyr Gly Asp Tyr Gly Gln Leu Gly Val
 210 215 220
 Gln Ala Leu Glu Glu Leu Ala Val Pro Arg Gly Ile Cys Val Ala Phe
 225 230 235 240
 Lys Asp Ile Val Pro Phe Ser Ala Arg Val Gly Asp Pro Arg Met Gln
 245 250 255
 Ser Met Met Gln His Leu Ala Gln Ala Arg Thr Thr Val Val Val Val
 260 265 270
 Phe Ser Asn Arg His Leu Ala Arg Val Phe Phe Arg Ser Val Val Leu
 275 280 285
 Ala Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Asp Trp Ala Ile
 290 295 300
 Ser Thr Tyr Ile Thr Ser Val Thr Gly Ile Gln Gly Ile Gly Thr Val
 305 310 315 320
 Leu Gly Val Ala Val Gln Gln Arg Gln Val Pro Gly Leu Lys Glu Phe
 325 330 335
 Glu Glu Ser Tyr Val Arg Ala Val Thr Ala Ala Pro Ser Ala Cys Pro
 340 345 350
 Glu Gly Ser Trp Cys Ser Thr Asn Gln Leu Cys Arg Glu Cys His Thr
 355 360 365
 Phe Thr Thr Arg Asn Met Pro Thr Leu Gly Ala Phe Ser Met Ser Ala
 370 375 380

Ala Tyr Arg Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly Leu His
 385 390 395 400
 Gln Leu Leu Gly Cys Thr Ser Glu Ile Cys Ser Arg Gly Pro Val Tyr
 405 410 415
 Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu Leu His
 420 425 430
 Glu Asn Thr Val Ala Phe Asp Asp Asn Gly Asp Thr Leu Gly Tyr Tyr
 435 440 445
 Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe Glu Ile
 450 455 460
 Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn Lys Thr
 465 470 475 480
 Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser Val Cys
 485 490 495
 Thr Thr Asp Cys Leu Ala Gly His His Arg Val Val Val Gly Ser His
 500 505 510
 His Cys Cys Phe Glu Cys Val Pro Cys Glu Ala Gly Thr Phe Leu Asn
 515 520 525
 Met Ser Glu Leu His Ile Cys Gln Pro Cys Gly Thr Glu Glu Trp Ala
 530 535 540
 Pro Lys Glu Ser Thr Thr Cys Phe Pro Arg Thr Val Glu Phe Leu Ala
 545 550 555 560
 Trp His Glu Pro Ile Ser Leu Val Leu Ile Ala Ala Asn Thr Leu Leu
 565 570 575
 Leu Leu Leu Leu Val Gly Thr Ala Gly Leu Phe Ala Trp His Phe His
 580 585 590
 Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu
 595 600 605
 Gly Ser Leu Val Ala Gly Ser Cys Ser Phe Tyr Ser Phe Phe Gly Glu
 610 615 620
 Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser Leu Gly
 625 630 635 640
 Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln Leu Val
 645 650 655
 Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr Arg Thr Trp
 660 665 670
 Ala Gln Asn His Gly Ala Gly Leu Phe Val Ile Val Ser Ser Thr Val
 675 680 685

His Leu Leu Ile Cys Leu Thr Trp Leu Val Met Trp Thr Pro Arg Pro
 690 695 700
 Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu Cys Thr
 705 710 715 720
 Glu Val Asn Ser Val Gly Phe Leu Leu Ala Phe Thr His Asn Ile Leu
 725 730 735
 Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu Leu Pro
 740 745 750
 Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Leu Asn
 755 760 765
 Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ala Ser Ile Tyr Gln Gly
 770 775 780
 Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Thr Thr Leu Ser
 785 790 795 800
 Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys
 805 810 815
 Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile Gln Asp
 820 825 830
 Tyr Thr Arg Arg Cys Gly Thr Thr
 835 840

<210> 17
 <211> 843
 <212> PRT
 <213> Rattus sp.

<400> 17
 Met Gly Pro Gln Ala Arg Thr Leu Cys Leu Leu Ser Leu Leu Leu His
 1 5 10 15
 Val Leu Pro Lys Pro Gly Lys Leu Val Glu Asn Ser Asp Phe His Leu
 20 25 30
 Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
 35 40 45
 Lys Ser Ile Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
 50 55 60
 Phe Thr Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
 65 70 75 80
 Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
 85 90 95
 Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile His
 100 105 110

Pro Gly Leu Tyr Phe Leu Ala Gln Asp Asp Asp Leu Leu Pro Ile Leu
 115 120 125
 Lys Asp Tyr Ser Gln Tyr Met Pro His Val Val Ala Val Ile Gly Pro
 130 135 140
 Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser His Phe
 145 150 155 160
 Leu Ile Pro Gln Ile Thr Tyr Ser Ala Ile Ser Asp Lys Leu Arg Asp
 165 170 175
 Lys Arg His Phe Pro Ser Met Leu Arg Thr Val Pro Ser Ala Thr His
 180 185 190
 His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp
 195 200 205
 Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His
 210 215 220
 Leu Leu Ser Gln Arg Leu Thr Lys Thr Ser Asp Ile Cys Ile Ala Phe
 225 230 235 240
 Gln Glu Val Leu Pro Ile Pro Glu Ser Ser Gln Val Met Arg Ser Glu
 245 250 255
 Glu Gln Arg Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser
 260 265 270
 Ala Arg Val Val Val Val Phe Ser Pro Glu Leu Ser Leu Tyr Ser Phe
 275 280 285
 Phe His Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala
 290 295 300
 Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu
 305 310 315 320
 Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile
 325 330 335
 Pro Gly Phe Ser Gln Phe Arg Val Arg Arg Asp Lys Pro Gly Tyr Pro
 340 345 350
 Val Pro Asn Thr Thr Asn Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp
 355 360 365
 Ala Cys Leu Asn Thr Thr Lys Ser Phe Asn Asn Ile Leu Ile Leu Ser
 370 375 380
 Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala
 385 390 395 400
 His Ala Leu His Arg Leu Leu Gly Cys Asn Arg Val Arg Cys Thr Lys
 405 410 415

Gln Lys Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn
 420 425 430
 Phe Thr Leu Leu Gly Asn Arg Leu Phe Phe Asp Gln Gln Gly Asp Met
 435 440 445
 Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Asp Leu Ser Gln Asn
 450 455 460
 Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Ser Lys Arg Leu Thr
 465 470 475 480
 Tyr Ile Asn Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Val
 485 490 495
 Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Ser Val
 500 505 510
 Gly Leu His Pro Cys Cys Phe Glu Cys Leu Asp Cys Met Pro Gly Thr
 515 520 525
 Tyr Leu Asn Arg Ser Ala Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly
 530 535 540
 Ser Met Trp Ser Tyr Lys Asn Asp Ile Thr Cys Phe Gln Arg Arg Pro
 545 550 555 560
 Thr Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Ala Ile Leu
 565 570 575
 Ala Ala Leu Gly Phe Phe Ser Thr Leu Ala Ile Leu Phe Ile Phe Trp
 580 585 590
 Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys
 595 600 605
 Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val
 610 615 620
 Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe
 625 630 635 640
 Phe Thr Val Cys Phe Ser Ile Cys Leu Ser Cys Ile Thr Val Arg Ser
 645 650 655
 Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala
 660 665 670
 Tyr Ser Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe
 675 680 685
 Ile Thr Ala Ile Lys Val Ala Leu Val Val Gly Asn Met Leu Ala Thr
 690 695 700
 Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Met
 705 710 715 720

Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
725 730 735

Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Met
740 745 750

Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
755 760 765

Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met
770 775 780

Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr
785 790 795 800

Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys
805 810 815

Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn
820 825 830

Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser
835 840

<210> 18

<211> 845

<212> PRT

<213> Rattus sp.

<400> 18

Met Val Arg Leu Leu Leu Ile Phe Phe Pro Met Ile Phe Leu Glu Met
1 5 10 15

Ser Ile Leu Pro Arg Met Pro Asp Arg Lys Val Leu Leu Ala Gly Ala
20 25 30

Ser Ser Gln Arg Ser Val Ala Arg Met Asp Gly Asp Val Ile Ile Gly
35 40 45

Ala Leu Phe Ser Val His His Gln Pro Pro Ala Glu Lys Val Pro Glu
50 55 60

Arg Lys Cys Gly Glu Ile Arg Glu Gln Tyr Gly Ile Gln Arg Val Glu
65 70 75 80

Ala Met Phe His Thr Leu Asp Lys Ile Asn Ala Asp Pro Val Leu Leu
85 90 95

Pro Asn Ile Thr Leu Gly Ser Glu Ile Arg Asp Ser Cys Trp His Ser
100 105 110

Ser Val Ala Leu Glu Gln Ser Ile Glu Phe Ile Arg Asp Ser Leu Ile
115 120 125

Ser Ile Arg Asp Glu Lys Asp Gly Leu Asn Arg Cys Leu Pro Asp Gly
130 135 140

Gln Thr Leu Pro Pro Gly Arg Thr Lys Lys Pro Ile Ala Gly Val Ile
 145 150 155 160
 Gly Pro Gly Ser Ser Ser Val Ala Ile Gln Val Gln Asn Leu Leu Gln
 165 170 175
 Leu Phe Asp Ile Pro Gln Ile Ala Tyr Ser Ala Thr Ser Ile Asp Leu
 180 185 190
 Ser Asp Lys Thr Leu Tyr Lys Tyr Phe Leu Arg Val Val Pro Ser Asp
 195 200 205
 Thr Leu Gln Ala Arg Ala Met Leu Asp Ile Val Lys Arg Tyr Asn Trp
 210 215 220
 Thr Tyr Val Ser Ala Val His Thr Glu Gly Asn Tyr Gly Glu Ser Gly
 225 230 235 240
 Met Asp Ala Phe Lys Glu Leu Ala Ala Gln Glu Gly Leu Cys Ile Ala
 245 250 255
 His Ser Asp Lys Ile Tyr Ser Asn Ala Gly Glu Lys Ser Phe Asp Arg
 260 265 270
 Leu Leu Arg Lys Leu Arg Glu Arg Leu Pro Lys Ala Arg Val Val Val
 275 280 285
 Cys Phe Cys Glu Gly Met Thr Val Arg Gly Leu Leu Ser Ala Met Arg
 290 295 300
 Arg Leu Gly Val Val Gly Glu Phe Ser Leu Ile Gly Ser Asp Gly Trp
 305 310 315 320
 Ala Asp Arg Asp Glu Val Ile Glu Gly Tyr Glu Val Glu Ala Asn Gly
 325 330 335
 Gly Ile Thr Ile Lys Leu Gln Ser Pro Glu Val Arg Ser Phe Asp Asp
 340 345 350
 Tyr Phe Leu Lys Leu Arg Leu Asp Thr Asn Thr Arg Asn Pro Trp Phe
 355 360 365
 Pro Glu Phe Trp Gln His Arg Phe Gln Cys Arg Leu Pro Gly His Leu
 370 375 380
 Leu Glu Asn Pro Asn Phe Lys Lys Val Cys Thr Gly Asn Glu Ser Leu
 385 390 395 400
 Glu Glu Asn Tyr Val Gln Asp Ser Lys Met Gly Phe Val Ile Asn Ala
 405 410 415
 Ile Tyr Ala Met Ala His Gly Leu Gln Asn Met His His Ala Leu Cys
 420 425 430
 Pro Gly His Val Gly Leu Cys Asp Ala Met Lys Pro Ile Asp Gly Arg
 435 440 445

Lys Leu Leu Asp Phe Leu Ile Lys Ser Ser Phe Val Gly Val Ser Gly
 450 455 460
 Glu Glu Val Trp Phe Asp Glu Lys Gly Asp Ala Pro Gly Arg Tyr Asp
 465 470 475 480
 Ile Met Asn Leu Gln Tyr Thr Glu Ala Asn Arg Tyr Asp Tyr Val His
 485 490 495
 Val Gly Thr Trp His Glu Gly Val Leu Asn Ile Asp Asp Tyr Lys Ile
 500 505 510
 Gln Met Asn Lys Ser Gly Met Val Arg Ser Val Cys Ser Glu Pro Cys
 515 520 525
 Leu Lys Gly Gln Ile Lys Val Ile Arg Lys Gly Glu Val Ser Cys Cys
 530 535 540
 Trp Ile Cys Thr Ala Cys Lys Glu Asn Glu Phe Val Gln Asp Glu Phe
 545 550 555 560
 Thr Cys Arg Ala Cys Asp Leu Gly Trp Trp Pro Asn Ala Glu Leu Thr
 565 570 575
 Gly Cys Glu Pro Ile Pro Val Arg Tyr Leu Glu Trp Ser Asp Ile Glu
 580 585 590
 Ser Ile Ile Ala Ile Ala Phe Ser Cys Leu Gly Ile Leu Val Thr Leu
 595 600 605
 Phe Val Thr Leu Ile Phe Val Leu Tyr Arg Asp Thr Pro Val Val Lys
 610 615 620
 Ser Ser Ser Arg Glu Leu Cys Tyr Ile Ile Leu Ala Gly Ile Phe Leu
 625 630 635 640
 Gly Tyr Val Cys Pro Phe Thr Leu Ile Ala Lys Pro Thr Thr Thr Ser
 645 650 655
 Cys Tyr Leu Gln Arg Leu Leu Val Gly Leu Ser Ser Ala Met Cys Tyr
 660 665 670
 Ser Ala Leu Val Thr Lys Thr Asn Arg Ile Ala Arg Ile Leu Ala Gly
 675 680 685
 Ser Lys Lys Lys Ile Cys Thr Arg Lys Pro Arg Phe Met Ser Ala Trp
 690 695 700
 Ala Gln Val Ile Ile Ala Ser Ile Leu Ile Ser Val Gln Leu Thr Leu
 705 710 715 720
 Val Val Thr Leu Ile Ile Met Glu Pro Pro Met Pro Ile Leu Ser Tyr
 725 730 735
 Pro Ser Ile Lys Glu Val Tyr Leu Ile Cys Asn Thr Ser Asn Leu Gly
 740 745 750

Val Val Ala Pro Val Gly Tyr Asn Gly Leu Leu Ile Met Ser Cys Thr
755 760 765

Tyr Tyr Ala Phe Lys Thr Arg Asn Val Pro Ala Asn Phe Asn Glu Ala
770 775 780

Lys Tyr Ile Ala Phe Thr Met Tyr Thr Thr Cys Ile Ile Trp Leu Ala
785 790 795 800

Phe Val Pro Ile Tyr Phe Gly Ser Asn Tyr Lys Ile Ile Thr Thr Cys
805 810 815

Phe Ala Val Ser Leu Ser Val Thr Val Ala Leu Gly Cys Met Phe Thr
820 825 830

Pro Lys Met Tyr Ile Ile Ile Ala Lys Pro Glu Arg Asn
835 840 845

<210> 19

<211> 867

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
1 5 10 15

Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
20 25 30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
35 40 45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
50 55 60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
65 70 75 80

Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
85 90 95

Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
100 105 110

Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
115 120 125

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
130 135 140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
145 150 155 160

Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
165 170 175

Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
 180 185 190
 Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
 195 200 205
 Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
 210 215 220
 Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
 225 230 235 240
 Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
 245 250 255
 Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
 260 265 270
 Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
 275 280 285
 Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
 290 295 300
 Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
 305 310 315 320
 Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
 325 330 335
 Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
 340 345 350
 Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
 355 360 365
 Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
 370 375 380
 Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
 385 390 395 400
 Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
 405 410 415
 Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
 420 425 430
 Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
 435 440 445
 Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
 450 455 460
 Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
 465 470 475 480

Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
 485 490 495
 Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
 500 505 510
 Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
 515 520 525
 Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
 530 535 540
 Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
 545 550 555 560
 Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
 565 570 575
 Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
 580 585 590
 Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp
 595 600 605
 Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile
 610 615 620
 Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr
 625 630 635 640
 Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe
 645 650 655
 Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro
 660 665 670
 Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe
 675 680 685
 Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu
 690 695 700
 Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly
 705 710 715 720
 Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile
 725 730 735
 Val Ile Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg
 740 745 750
 Asn Gln Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly
 755 760 765
 Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala
 770 775 780

Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn
 785 790 795 800

Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile
 805 810 815

Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe
 820 825 830

Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu
 835 840 845

Leu Ala Cys Ile Phe Phe Asn Lys Ile Tyr Ile Ile Leu Phe Lys Pro
 850 855 860

Ser Arg Asn
 865